Automatic Quantification of P-Wave Morphological Features

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INTRODUCTION

Atrial fibrillation (AF) is the most frequently occurring sustained cardiac rhythm disturbance (Wolf, Mitchell, Baker, Kannel, & D'Agostino, 1998). Although relatively easy to diagnose by analysis of the surface ECG, AF has modalities, mechanisms, and predisposing conditions that still remain poorly understood.

AF is not a direct life-threatening arrhythmia. However, because of the associated strong symptomatology, it frequently results in hospitalisation, physician visits, and drug therapy, hereby limiting the physical and social activities of many patients. It not only affects the quality of life, but it also increases the likelihood of prothrombotic effects and the risk for mortality because of cerebrovascular events or progressive ventricular dysfunction (Wolf et al., 1998).

AF is also a frequent post-cardiosurgery complication that results in an increase of length of hospital stay and of the associated costs (Kannel, Wolf, Benjamin, & Levy, 1998). Even though several underlying pathophysiological conditions might predispose to AF, no reliable method exists as yet to stratify the relative risk for AF development from a patient's clinical state, or by analysis of the available bedside data (Gang, Hnatkova, Mandal, Ghuran, & Malik, 2004). It is not possible to predict episode recurrence in paroxysmal patients, since AF can often be asymptomatic, nor does a method to identify patients at risk for post-cardiosurgery AF by pre-operative clinical investigations exist.

In the last decades, several studies have focused on finding reliable methods for the prediction of atrial fibrillation by analysis of surface electrocardiographic records. The ECG is a simple and widely available noninvasive technique used in the diagnosis of various cardiac diseases. The P-wave represents the sequential atrial activation of right and left atria, and it reflects the atrial conduction properties. Indeed, individuals with a clinical history of paroxysmal AF have a longer inter-atrial and intra-atrial conduction time, shown as a P-wave prolongation on the surface ECG. Moreover, the regional differences in atrial activation time in AF patients might be reflected in temporal variations across the leads of an orthogonal ECG (Villani, Piepoli, Rosi, & Capucci, 1996).

These findings have lead to an increasing interest in time domain P-wave analysis as a tool for AF risk stratification. Maximum P-wave (i.e., longest P-wave in a 12-lead ECG) and P-wave dispersion (difference between the longest and the shortest P-wave duration in 12-lead ECG) are currently the most sensitive indexes for AF risk assessment (Dilaveris & Gialafos, 2001). However, time domain methods are limited by the lack of a standard and accepted definition of P-wave duration. P-wave boundaries are difficult to detect, both because of the small amplitude of the atrial signal on the ECG, and because of the gradual slope of the atrial waveform from the baseline. For this reason, its determination is mainly attributed to the cardiologist's opinion and experience. Obviously, this reduces the applicability

of time domain indexes in AF risk stratification, since cut-off values result to be dependent on the particular study group, the patient population investigated, and also the technological equipment used.

Nevertheless, irregularities of P-wave morphology have been detected in patients with paroxysmal atrial fibrillation (Dilaveris & Gialafos, 2002), and different shapes of P-wave may represent the presence or absence of an underlying pathophysiological condition in patients prone to AF attacks (Carlson, Johansson, & Olsson, 2001). Indeed, P-wave morphological analysis can help detecting interatrial blocks, which predispose to this cardiac rhythm disturbance, even in patients who develop AF despite the absence of particular alterations in echocardiographic parameters (Bayes de Luna, Guindo, Vinolas, Martinez-Rubio, Oter, & Bayes-Genis, 1999).

BACKGROUND

Morphological analysis of P-wave has been extensively used to assess interatrial conduction defects and abnormalities of the left and right atrium (Dilaveris & Gialafos, 2002; Michelucci, Bagliani, Colella, Pieragnoli, Porciani, Gensini, Padeletti, 2002; Platonov, Carlson, Ingemansson, Roijer, Hansson, Chireikin, & Olsson, 2000). Changes in P-wave polarity, as well as subtle differences in P-wave morphology, are believed to reflect abnormal activation patterns in the atria (Michelucci et al., 2002). Irregularities in the orthogonal P-wave morphology have been detected in AF patients and associated with local interatrial conduction delay (Platonov et al., 2000). Different shapes of P-wave have been shown to represent the presence or absence of an underlying pathophysiological condition in patients prone to AF attacks (Gang et al., 2004). In the presence of a partial inter-atrial conduction block, P-wave shape changes have been demonstrated to depend on the direction of the activation wavefront. The studies on P-wave morphology are usually performed by visual inspection of shape changes. However, abnormalities of left or right atrium are likely reflected in subtle morphological changes beyond visual classification.

We hereby present a P-wave model, based on a linear combination of Gaussian functions, to perform an automatic and reliable quantification of the morphological features of P-wave in patients with paroxysmal atrial fibrillation (Censi et al., 2007). In addition, given the importance of multichannel electrocardiography for the extraction of quantitative parameters, we used a 32-lead mapping ECG system, to increase the spatial sampling on the body surface and to enhance low amplitude signals (Trobec, 2003).

MORPHOLOGICAL ANALYSIS OF THE P-WAVE

In order to overcome the limitations related to the time-domain analysis, an automated morphological analysis of the P-wave can be obtained by a model based on a Gaussian fit of averaged P-wave. Such a model can numerically and automatically quantify, beyond visual inspection, morphological aspects of P- wave in AF patients.

By describing a P-wave as a linear combination of up to eight Gaussian functions, the number of Gaussians that explain 97.5% of the signal variance is used as representative of that specific wave. The fit, in a way, acts as a filter that eliminates high-frequency noise.

Since more than one Gaussian function can be used by the model to cover steep portions of the signal, without really fitting a peak or valley, a better morphological description of the wave is obtained by evaluating the number of *maxima*, *minima,* and *zeroes* of the extracted fit. The P-wave morphology is then evaluated by the following parameters: the model order at which AdjRsq≥97.5%; the minimum (σ_{min}) standard deviation of the Gaussians included in the model; the maximum (σ_{max}) standard deviation of the Gaussians included in the model; the number of relative maxima and minima (max+min); and the number of zero crossings of the model (zeros). The Gaussian fitting of two P-waves with different morphology is shown in Figure 2. The P-wave on the left achieves an AdjRsq = 98.93% with a second first order model (two Gaussian functions), while in the second case, AdjRsq higher than 97.5% is only reached with a 6^{th} order Gaussian fit. Lower panel shows the values of the five parameters extracted from the Gaussian fit to quantify the morphological features.

The parameters chosen synthesise the main morphological characteristics of the original waveforms: the order of the model is the number of Gaussians required; the number of maxima and minima provides information on the number of 'bumps' included in the waveform; the number of zeros accounts for the phase changes of the P-wave.